SEQUENCE LISTING

<110> Medical & Biological Laboratories Co.,Ltd.

<120> Thioredoxin reductase II

<130> M3-007PCT

<140>

<141>

<150> JP 1998-310422

<151> 1998-10-30

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 1959

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(1572)

<220>

<221> misc_structure

<222> (1567)..(1569)

<220>

<221> misc_structure

<222> (1664)..(1666)

<223> tga is transrated to selenosysteine, shown by Xaa.

<400> 1

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atggcggca atg gcg gtg gcg ctg cgg gga tta gga ggg cgc ttc cgg tgg 51
          Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp
            1               5                  10

cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca   99
Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
 15                  20                  25                  30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct  147
Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser
                35                  40                  45

ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg  195
Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
            50                  55                  60

gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc  243
Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
        65                  70                  75

ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg  291
Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
    80                  85                  90

cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat  339
His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr
 95                  100                 105                 110

ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca  387
Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala
                115                 120                 125
```

```
gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc   435
Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val
            130                 135                 140

cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt   483
Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe
        145                 150                 155

gtt gac gag cac acg gtt tgc ggc gtt gcc aaa ggt ggg aaa gag att   531
Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile
    160                 165                 170

ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga   579
Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg
175                 180                 185                 190

tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat   627
Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp
                195                 200                 205

gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg   675
Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly
            210                 215                 220

gcc agc tat gtg gcc ctg gag tgt gct ggc ttc ctc acc ggg att ggg   723
Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly
        225                 230                 235

ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac   771
Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp
    240                 245                 250

cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc   819
Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr
255                 260                 265                 270
```

```
cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc agg agg ctc cct gat   867
Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp
                275                 280                 285

ggc cag ctg cag gtc acc tgg gag gac agc acc acc ggc aag gag gac   915
Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp
            290                 295                 300

acg ggc acc ttt gac acc gtc ctg tgg gcc ata ggt cga gtc cca gac   963
Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
        305                 310                 315

acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac   1011
Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
    320                 325                 330

act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac   1059
Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
335                 340                 345                 350

atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc   1107
Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
                355                 360                 365

aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg   1155
Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
            370                 375                 380

tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc   1203
Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
        385                 390                 395

cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct   1251
Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
    400                 405                 410
```

```
cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca   1299
Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
415                 420                 425                 430

ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag   1347
Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
                435                 440                 445

atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc   1395
Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
            450                 455                 460

ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc   1443
Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
        465                 470                 475

aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat   1491
Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
    480                 485                 490

ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca   1539
Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
495                 500                 505                 510

ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc 1592
Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
                515                 520

cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc agacccagga tggctgcagg 1652

ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt gagatggtca gcgtggagcg 1712

caagtgctgg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc 1772

accctgcac ctttcagcct ttgccgccgg gcacccccc caggctcctg gtgccggatg 1832
```

atgacgacct gggtggaaac ctaccctgtg ggcacccatg tccgagcccc ctggcatttc 1892

tgcaatgcaa ataaagaggg tacttttttct gaagtgtgta aaaaaaaaaa aaaaaaaaaa 1952

aaaaaaa 1959

<210> 2
<211> 521
<212> PRT
<213> Homo sapiens
<223> Xaa(520) means selenosysteine.

<400> 2

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Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp Arg Thr
  1               5                  10                  15

Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala Ala Ala
             20                  25                  30

Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly
         35                  40                  45

Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
     50                  55                  60

Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
 65                  70                  75                  80

Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
                 85                  90                  95

Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
            100                 105                 110

Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
```

```
        115                 120                 125

Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
    130                 135                 140

Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
145                 150                 155                 160

Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu
                165                 170                 175

Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro
            180                 185                 190

Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile
        195                 200                 205

Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser
    210                 215                 220

Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp
225                 230                 235                 240

Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln
                245                 250                 255

Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe
            260                 265                 270

Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln
        275                 280                 285

Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly
    290                 295                 300

Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg
```

305 310 315 320

Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
325 330 335

Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
340 345 350

Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
355 360 365

Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
370 375 380

Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
385 390 395 400

Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
405 410 415

Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
420 425 430

Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
435 440 445

Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
450 455 460

Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
465 470 475 480

Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
485 490 495

Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu

500 505 510

Asp Pro Thr Val Thr Gly Cys Xaa Gly
515 520

<210> 3
<211> 2056
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)..(1669)
<223> tga(1664)..(1666) is transrated to selenosysteine, shown by Xaa.

<400> 3
gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60

ttctccatcc ctccctttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229
Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
1 5 10

gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag 277
Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
15 20 25 30

ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa 325
Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
35 40 45

ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc 373

```
Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
            50                  55                  60

ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa   421
Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
        65                  70                  75

gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac   469
Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
    80                  85                  90

tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac   517
Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
95                  100                 105                 110

tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac   565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn
                115                 120                 125

atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa   613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys
            130                 135                 140

ggt ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act   661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr
        145                 150                 155

gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat   709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr
    160                 165                 170

gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa   757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys
175                 180                 185                 190

acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc   805
```

```
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
                195                 200                 205

ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc   853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro
            210                 215                 220

ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg   901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met
        225                 230                 235

gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc   949
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val
    240                 245                 250

agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc   997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr
255                 260                 265                 270

acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata  1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile
                275                 280                 285

ggt cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta  1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val
            290                 295                 300

gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc  1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala
        305                 310                 315

acc tct gtg ccc cac atc tac gcc att ggt gac gtg gtg gag ggg cgg  1189
Thr Ser Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg
    320                 325                 330

cct gag ctg aca ccc aca gcg atc atg gcc ggg agg ctc ctg gtg cag  1237
```

```
Pro Glu Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln
335                 340                 345                 350

cgg ctc ttc ggc ggg tcc tca gat ctg atg gac tac gac aat gtt ccc   1285
Arg Leu Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro
                355                 360                 365

acg acc gtc ttc acc cca ctg gag tat ggc tgt gtg ggg ctg tcc gag   1333
Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu
            370                 375                 380

gag gag gca gtg gct cgc cac ggg cag gag cat gtt gag gtc tat cac   1381
Glu Glu Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His
        385                 390                 395

gcc cat tat aaa cca ctg gag ttc acg gtg gct gga cga gat gca tcc   1429
Ala His Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser
    400                 405                 410

cag tgt tat gta aag atg gtg tgc ctg agg gag ccc cca cag ctg gtg   1477
Gln Cys Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val
415                 420                 425                 430

ctg ggc ctg cat ttc ctt ggc ccc aac gca ggc gaa gtt act caa gga   1525
Leu Gly Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly
                435                 440                 445

ttt gct ctg ggg atc aag tgt ggg gct tcc tat gcg cag gtg atg cgg   1573
Phe Ala Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg
            450                 455                 460

acc gtg ggt atc cat ccc aca tgc tct gag gag gta gtc aag ctg cgc   1621
Thr Val Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg
        465                 470                 475

atc tcc aag cgc tca ggc ctg gac ccc acg gtg aca ggc tgc tga ggg   1669
```

Ile Ser Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
480 485 490

taagcgccat ccctgcaggc cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc 1729

agacccagga tggctgcagg ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt 1789

gagatggtca gcgtggagcg caagtgctgg acgggtggcc cgtgtgcccc acagggatgg 1849

ctcaggggac tgtccacctc acccctgcac ctttcagcct ttgccgccgg gcacccccc 1909

caggctcctg gtgccggatg atgacgacct gggtggaaac ctaccctgtg ggcacccatg 1969

tccgagcccc ctggcatttc tgcaatgcaa ataaagaggg tacttttttct gaagtgtgta 2029

aaaaaaaaaa aaaaaaaaaa aaaaaaa 2056

<210> 4
<211> 492
<212> PRT
<213> Homo sapiens
<223> Xaa(493) means selenosysteine.

<400> 4
Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly
1 5 10 15

Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly
20 25 30

Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr
35 40 45

Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys
50 55 60

```
Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
 65                  70                  75                  80

Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
                 85                  90                  95

Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
            100                 105                 110

His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
        115                 120                 125

Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
    130                 135                 140

Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
145                 150                 155                 160

Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
                165                 170                 175

Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
            180                 185                 190

Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
        195                 200                 205

Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
    210                 215                 220

Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser
225                 230                 235                 240

His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
                245                 250                 255
```

```
Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
            260                 265                 270

Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
        275                 280                 285

Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
    290                 295                 300

Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
305                 310                 315                 320

Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
                325                 330                 335

Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
            340                 345                 350

Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
        355                 360                 365

Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
    370                 375                 380

Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
385                 390                 395                 400

Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
                405                 410                 415

Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
            420                 425                 430

Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
        435                 440                 445
```

Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
450 455 460

Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser
465 470 475 480

Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
485 490

<210> 5
<211> 130
<212> DNA
<213> Homo sapiens

<400> 5
tcagcctttg ccgccgggca ccccccccag gctcctggtg ccggatgatg acgacctggg 60

tggaaaccta ccctgtgggc acccatgtcc gagccccctg gcatttctgc aatgcaaata 120

aagagggtac 130

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 6
gcgggatcca tgacttttaa cagttttgaa gg 32

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 7

gcgctcgagc tactatagag ttagattaag ac 32

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 8

tatgatctcc tggtggtc 18

<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthesis

<400> 9

gtcatcactt gtgattcc 18

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 10
acagcttctg ccatcttcct c 21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 11
agaaggttcc acgtagtcca c 21

<210> 12
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence:Synthesis

<400> 12
ccatacgatg ttccagatta c 21

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthesis

<400> 13

acgatggcgg caatggcggt g 21

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthesis

<400> 14

accatggagg accaagcagg t 21

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 15

ttaccctcag cagcctgtca c 21

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 16

gcgccatccc tgcaggccag g 21

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 17

cacacttcag aaaaagtacc c 21

<210> 18

<211> 103

<212> DNA

<213> Homo sapiens

<400> 18

atggcggcaa tggcggtggc gctgcgggga ttaggagggc gcttccggtg gcggacgcag 60

gccgtggcgg gcggggtgcg gggcgcggcg cggggcgcag cag 103

<210> 19

<211> 200

<212> DNA

<213> Homo sapiens

<400> 19

gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60

ttctccatcc ctccctttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

agccaccatg gaggaccaag 200

<210> 20

<211> 69

<212> DNA

<213> Homo sapiens

<400> 20

caggtcagcg ggactatgat ctcctggtgg tcggcggggg atctggtggc ctggcttgtg 60

ccaaggagg 69

<210> 21

<211> 57

<212> DNA

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